

FIG. 1

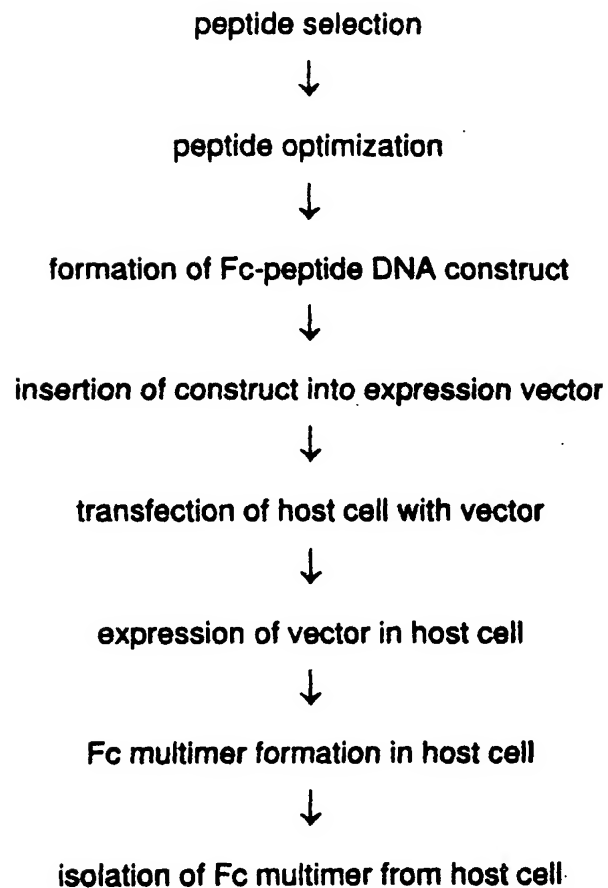


FIG. 2A

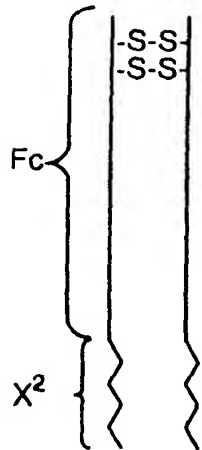


FIG. 2B

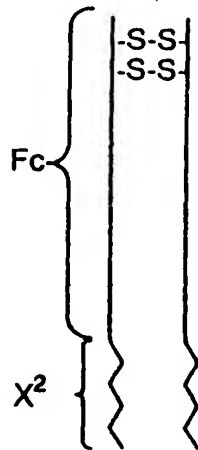


FIG. 2C

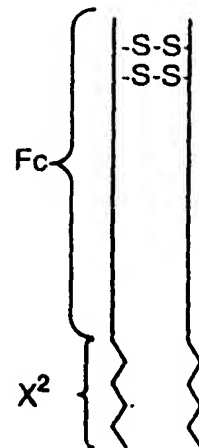


FIG. 2D

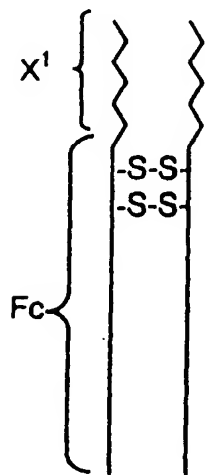


FIG. 2E

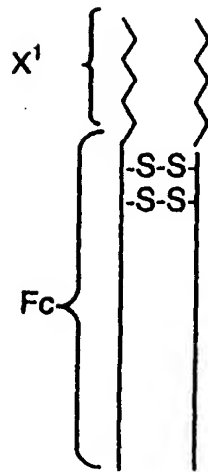


FIG. 2F

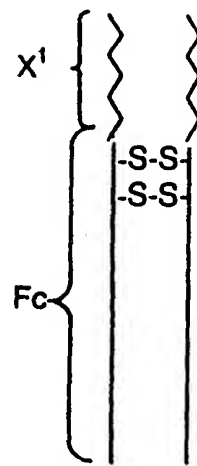


FIG. 3A

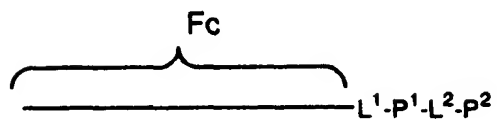


FIG. 3B

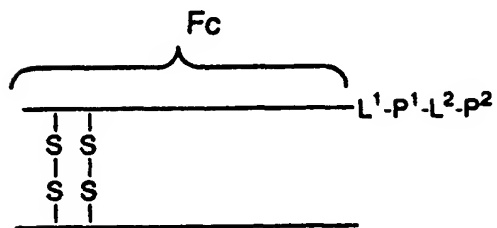


FIG. 3C

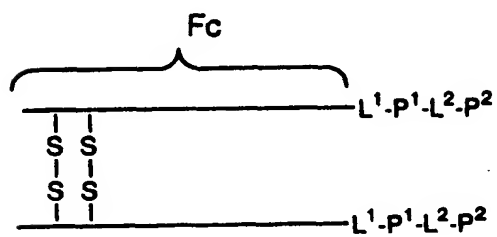


FIG. 4

```

ATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCCTTGAGGACCCCCCTGGCAGT

a      M D K T H T C P P C P A P E L L G G P S .

GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a      V F L F P P K P K D T L M I S R T P E V .

ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a      T C V V V D V S H E D P E V K F N W Y V .

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGG
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCGTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a      D G V E V H N A K T K P R E E Q Y N S T .

TACCGTGTGGTCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATG

a      Y R V V S V L T V L H Q D W L N G K E Y .

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCC
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCAGAGGTTGTTTCGGGAGGGTTCGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a      K C K V S N K A L P A P I E K T I S K A .

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a      K G Q P R E P Q V Y T L P P S R D E L T .

AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a      K N Q V S L T C L V K G F Y P S D I A V .

GAGTGGGAGAGCAATGGGCAGCCGGAACAACATAAGACCACGCCTCCCGTGTCTGGAC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
CTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGACGACCTG

a      E W E S N G Q P E N N Y K T T P P V L D .

TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a      S D G S F F L Y S K L T V D K S R W Q Q .

GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTGTCGCTCTTC

a      G N V F S C S V M H E A L H N H Y T Q K .

AGCCTCTCCCTGTCTCCGGGTAAA
661 -----+-----+-----+-----+-----+-----+-----+-----+ 684
TCGGAGAGGGACAGAGGCCCATTT

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FIG. 5

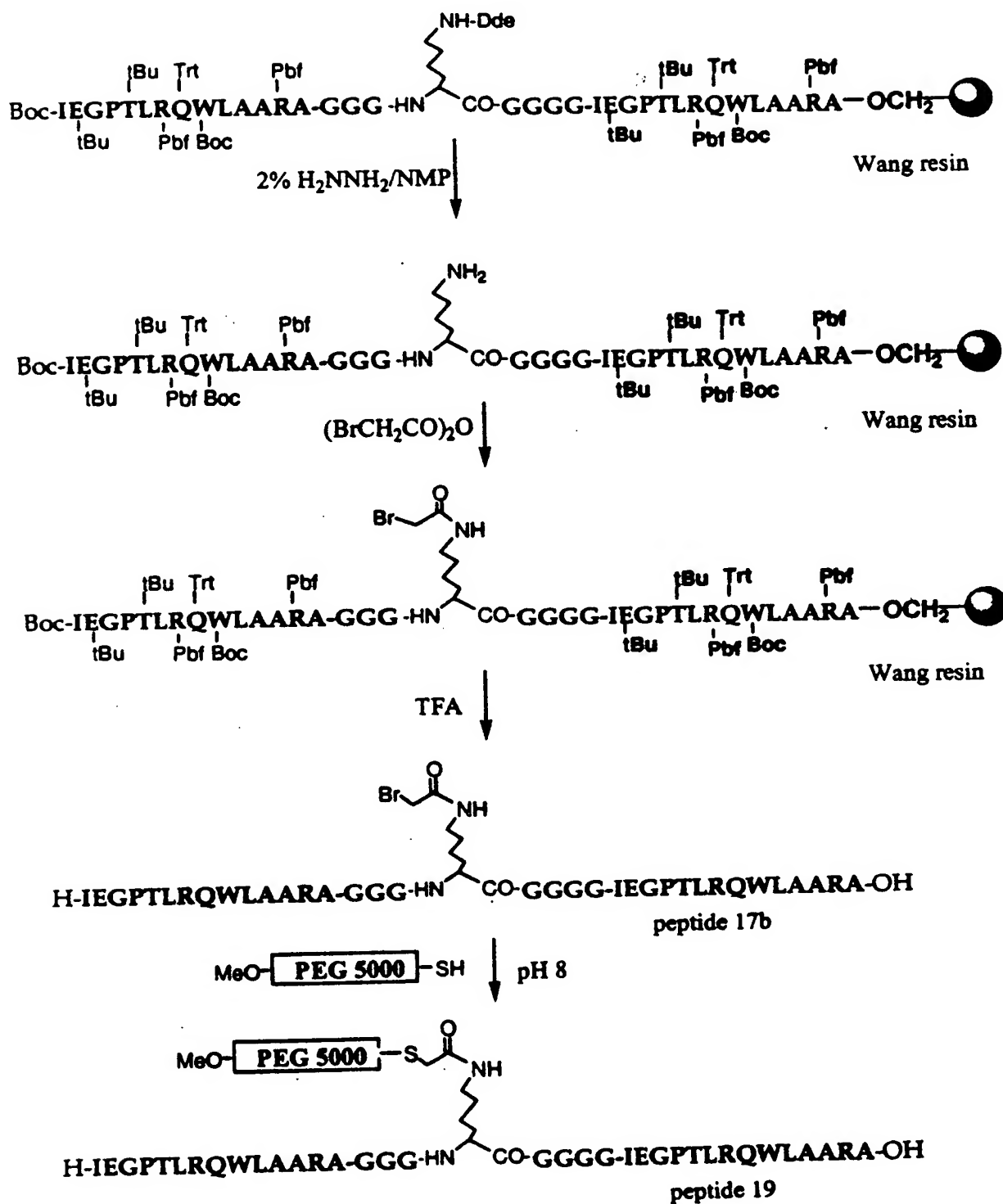
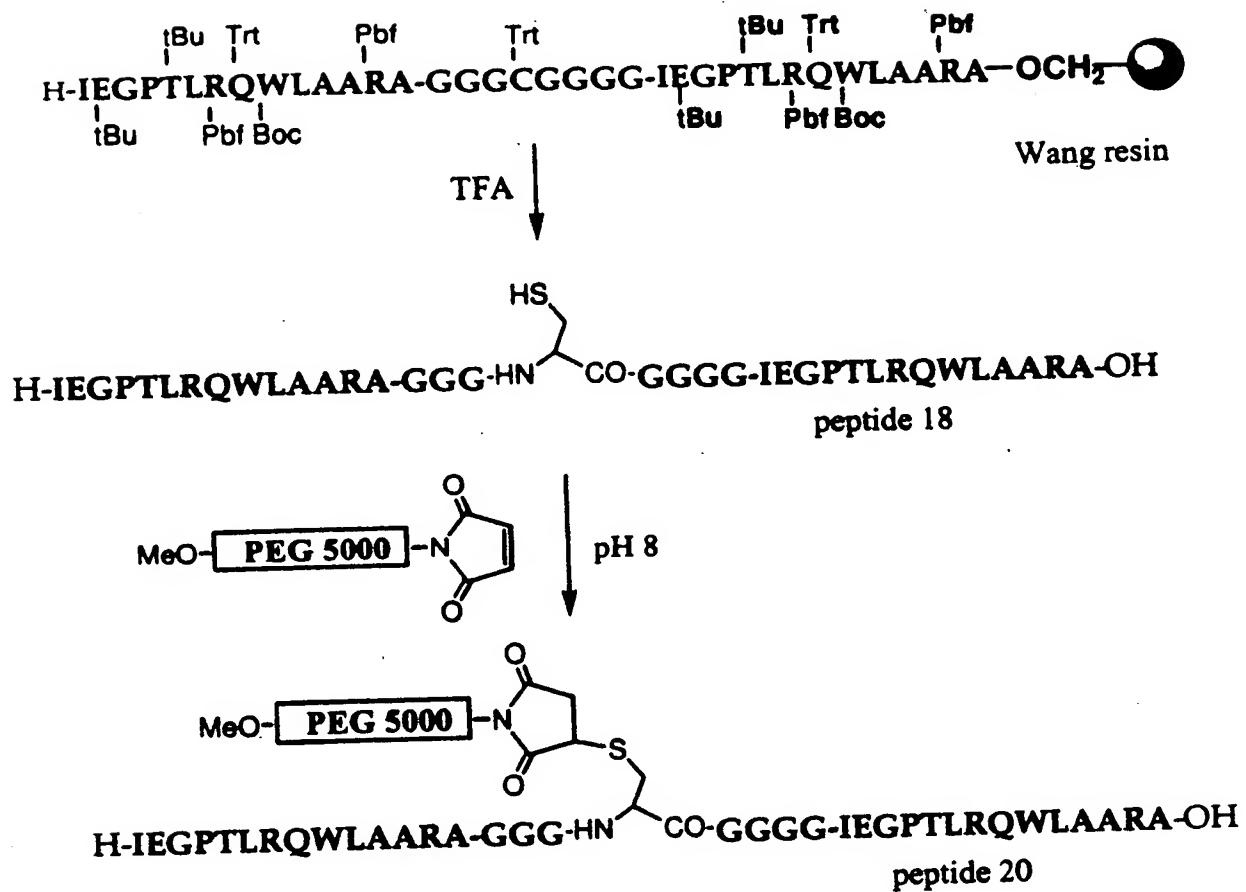


FIG. 6



[illegible]

FIG. 9

XbaI
|
TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC
1+..... 60
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG
c M I E G P T L R -

GTCAGTGGCTGGCTGCTCGTGCTGGCGGTGGTGGCGGAGGGGGTGGCATTGAGGGCCCAA
61+..... 120
CAGTCACCGACCGACGAGCACGACCGCCACCACCGCTCCCCACCGTAACCTCCGGGTT
c Q W L A A R A G G G G G G G G I E G P T -

CCCTTCGCCAATGGCTTGCAGCACCGCAGGGGAGGCGGTGGGGACAAAACCTCACACAT
121+..... 180
GGGAAGCGGTTACCGAACGTCTGCGCGTCCCCCTCGGCCACCCCTGTTTTGAGTGTGTA
c L R Q W L A A R A G G G G G G D K T H T C -

GTCCACCTTGCCACGACCTGAACTCCTGGGGGACCGTCAGTTTTCTCTCCCCCCAA
181+..... 240
CAGGTGGAACGGTCTGAGCTTGAAGACCCCTGGCAGTCAAAGGAGAAGGGGGGTT
c P P C P A P E L L G G P S V F L F P P K -

AACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACG
241+..... 300
TTGGGTTCTGTGGAGTACTAGAGGCGCTGGGACTCCAGTGTACGCACCACCACTGC
c P K D T L M I S R T P E V T C V V V D V -

TGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATA
301+..... 360
ACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTAT
c S H E D P E V K P N W Y V D G V E V H N -

ATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCTCAGCGTCC
361+..... 420
TACGGTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCACTCGCAGG
c A K T K P R E E Q Y N S T Y R V V S V L -

TCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
421+..... 480
AGTGGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTACGTTCCAGAGGTTGT
c T V L H Q D W L N G K E Y K C K V S N K -

AAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAAC
481+..... 540
TTCCGGAGGGTCCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCCGGGCTCTTG
c A L P A P I E K T I S K A K G Q P R E P -

CACAGGTGTACACCCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCCTGA
541+..... 600
GTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACT
c Q V Y T L P P S R D E L T K N Q V S L T -

CCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC
601+..... 660
GGACGGACCAAGTTTCCGAAGATAGGGTCTGTAGCGGCACCTCACCCCTCTCGTTACCCG
c C L V K G F Y P S D I A V E W E S N G Q -

AGCCGGAGAACTACAAGACCACGCTCCCGTGGTGGACTCCGACGGCTCCTTCTTCC
661+..... 720
TCGGCCTCTTGTGATGTTCTGGTGGGAGGGACGACCTGAGGCTGCCGAGGAAGAAGG
c P E N N Y K T T P P V L D S D G S F F L -

TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCT
721+..... 780
AGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCTGTCAGAGAGTACGA
c Y S K L T V D K S R W Q Q G N V F S C S -

CCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
781+..... 840
GGCACTACGTAAGTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCC
c V M H E A L H N H Y T Q K S L S L S P G -

BamHI
|
GTAAATAATGGATCC
841+..... 855
CATTATTACCTAGG
c K *

XbaI
|

1 TCTAGATTGTGTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC 60
.....+.....+.....+.....+.....+
AGATCTAAACAAATGATTAATTTCTCTCTTATTGTATACTAGCTTCCAGGCTGAGACG
M I E G P T L R

61 GTCAGTGGCTGGCTGCTCGTGCTGGTGGAGGCGGTGGGGACAAAACCTCACACATGTCCAC 120
.....+.....+.....+.....+.....+
CAGTCACCGACCGACGAGCAGCACCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG
Q W L A A R A G G G G G D K T H T C P P

121 CTTGCCACGACCTGAACTCTCTGGGGGGACCGTCAGTTTTCTCTTCCCCCCTAAAACCCA 180
.....+.....+.....+.....+.....+
GAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGT
C P A P E L L G G P S V F L F P P K P K

181 AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC 240
.....+.....+.....+.....+.....+
TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG
D T L M I S R T P E V T C V V V D V S H

241 ACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA 300
.....+.....+.....+.....+.....+
TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT
E D P E V K F N W Y V D G V E V H N A K

301 AGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACC 360
.....+.....+.....+.....+.....+
TCTGTTTCGGCGCCCTCTCTCGTCATGTTGTCGTGCATGGCACACCACTCGCAGGAGTGGC
T K P R E E Q Y N S T Y R V V S V L T V

361 TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC 420
.....+.....+.....+.....+.....+
AGGACGTGGTCTCTGACCGACTTACCGTTCTCTCATGTTACGTTCCAGAGGTTGTTTCGGG
L H Q D W L N G K E Y K C K V S N K A L

421 TCCCAGCCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGG 480
.....+.....+.....+.....+.....+
AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCC
P A P I E K T I S K A K G Q P R E P Q V

481 TGTACACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCC 540
.....+.....+.....+.....+.....+
ACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGG
Y T L P P S R D E L T K N Q V S L T C L

541 TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG 600
.....+.....+.....+.....+.....+
ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCC
V K G F Y P S D I A V E W E S N G Q P E

601 AGAACAACCTACAAGACCACGCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACA 660
.....+.....+.....+.....+.....+
TCTTGTGTGATGTTCTGGTGGGAGGGCAGCAGCTGAGGCTGCCGAGGAAGAAGGAGATGT
N N Y K T T P P V L D S D G S F F L Y S

661 GCAAGCTCACCGTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA 720
.....+.....+.....+.....+.....+
CGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGCACT
K L T V D K S R W Q Q G N V F S C S V M

721 TGCATGAGGCTCTGCACAACCACTACACGCAGAAGACCTCTCCCTGTCTCCGGGTAAAT 780
.....+.....+.....+.....+.....+
ACGTA TCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTA
H E A L H N H Y T Q K S L S L S P G K

BamHI
|

781 AATGGATCC 789
TTACCTAGG

FIG.11

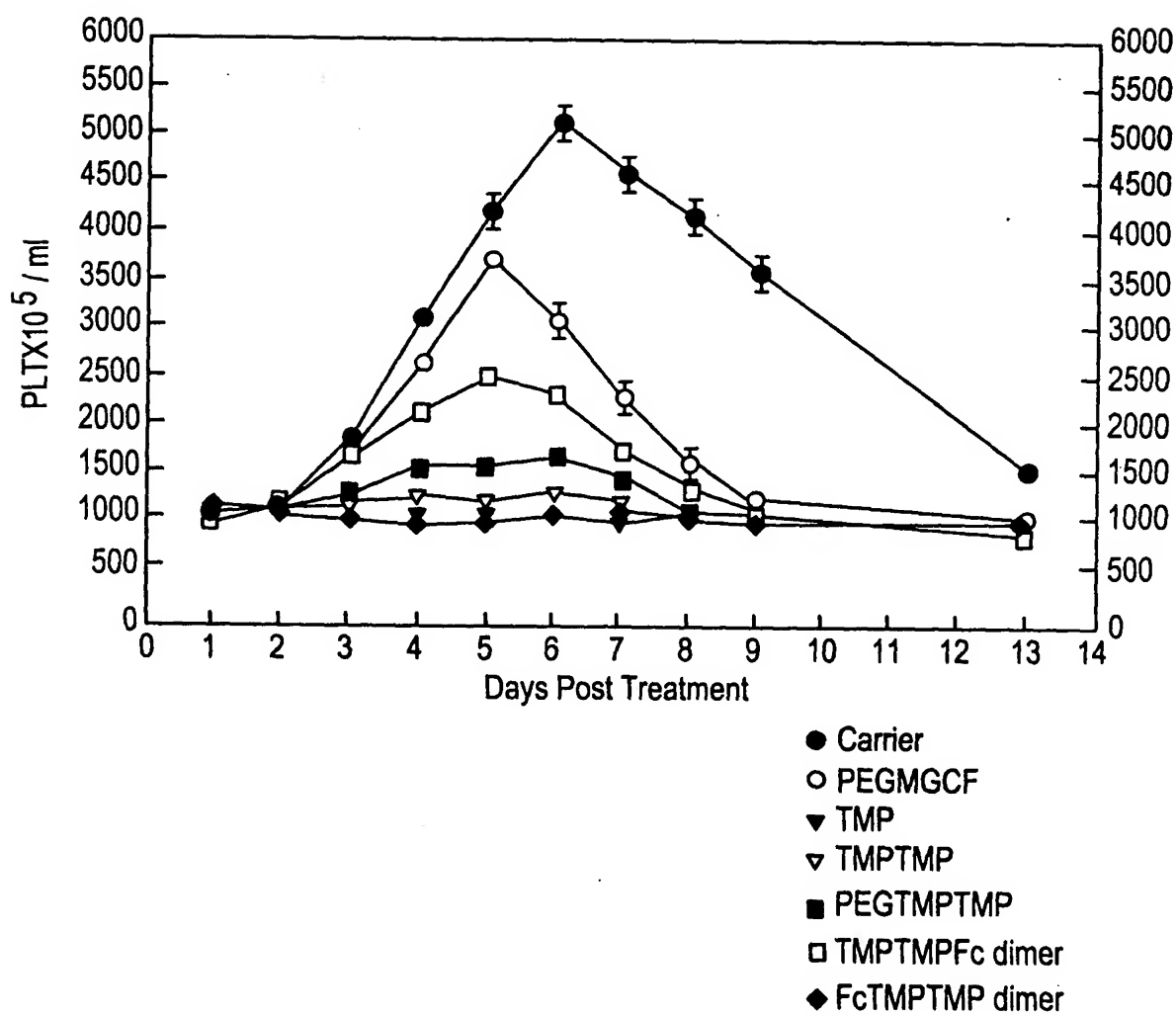


FIG.12

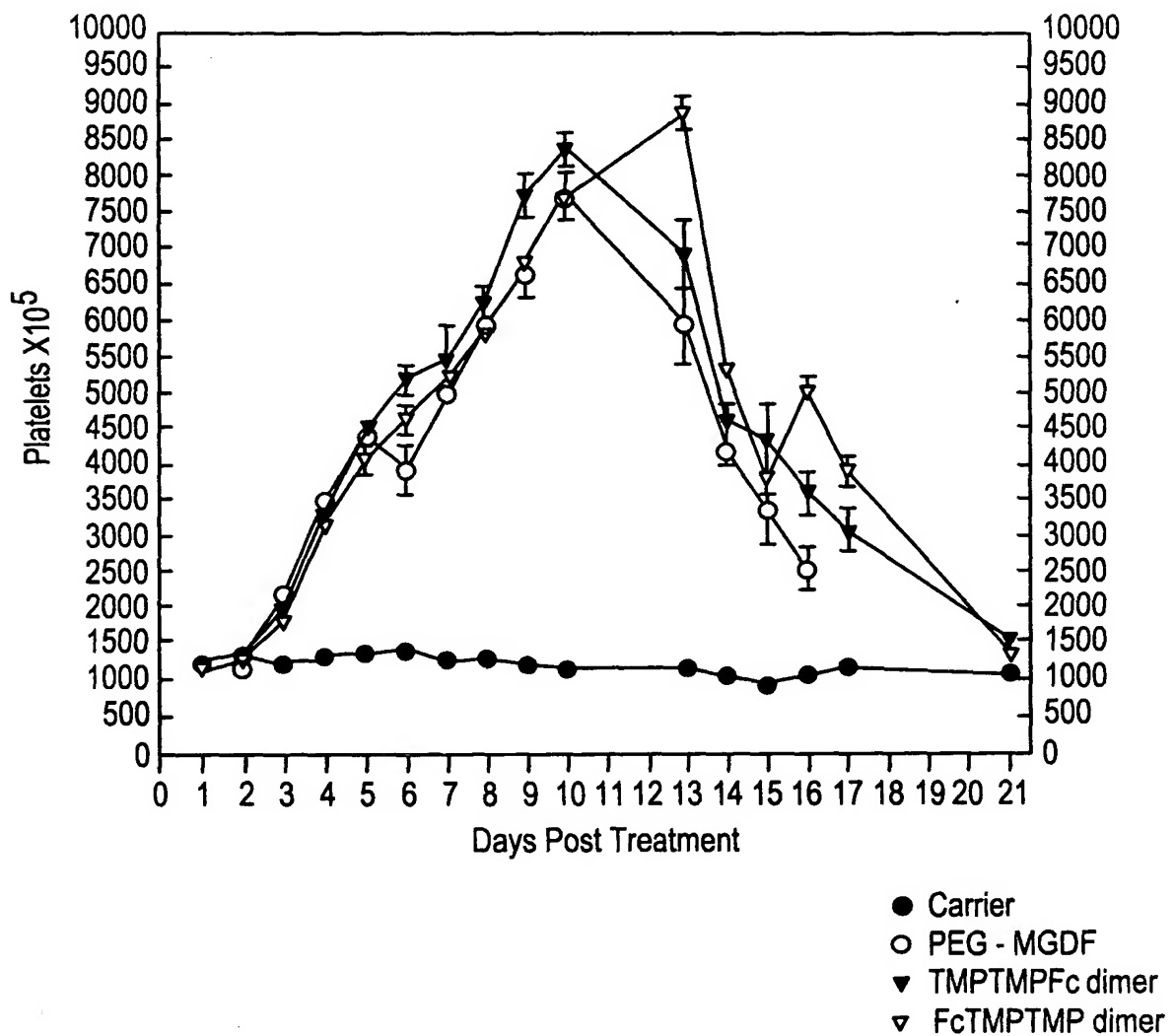


FIG. 13

XbaI
|

1 TCTAGATTGTTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG
CACCTTGTCCAGCTCCGGAACCTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAC
61 GTGGAACAGGTCGAGGCCCTTGAGGACCCCTGGCAGTCAGAAGGAGAAGGGGGTTTTG 120
P C P A P E L L G G P S V F L F P P K P
CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
121 GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCAC 180
K D T L M I S R T P E V T C V V V D V S
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
181 CCGTGTCTTCTGGGACTCCAGTTCAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC 240
H E D P E V K F N W Y V D G V E V H N A
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCA
241 GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT 300
K T K P R E E Q Y N S T Y R V V S V L T
CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG
301 GGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTTACGTTCCAGAGGTGTGTTT 360
V L H Q D W L N G K E Y K C K V S N K A
CCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
361 GGGAGGGTCCGGGGTAGTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG 420
L P A P I E K T I S K A K G Q P R E P Q
AGGTGTACACCCTGCCCCCATCCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
421 TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA 480
V Y T L P P S R D E L T K N Q V S L T C
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
481 CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG 540
L V K G F Y P S D I A V E W E S N G Q P
CGGAGAACAACCTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCCTCT
541 GCCTCTTGTGTGATGTTCTGGTCCGGAGGGCAGGACCTGAGGCTGCCGAGGAAGAAGGAGA 600
E N N Y K T T P P V L D S D G S F F L Y
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
601 TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCTTGCAGAAGAGTACGAGGC 660
S K L T V D K S R W Q Q G N V F S C S V
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
661 ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT 720
M H E A L H N H Y T Q K S L S L S P G K
AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCGCTGACTTGGGTTT
721 TTCCACCTCCACCACCCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAA 780
G G G G G G G T Y S C H F G P L T W V C
BamHI
|

781 GCAAACCGCAGGGTGGTTAATCTCGTGGATCC 812
CGTTTGGCGTCCCACCAATTAGAGCACCTAGG
K P O G G *

FIG. 14

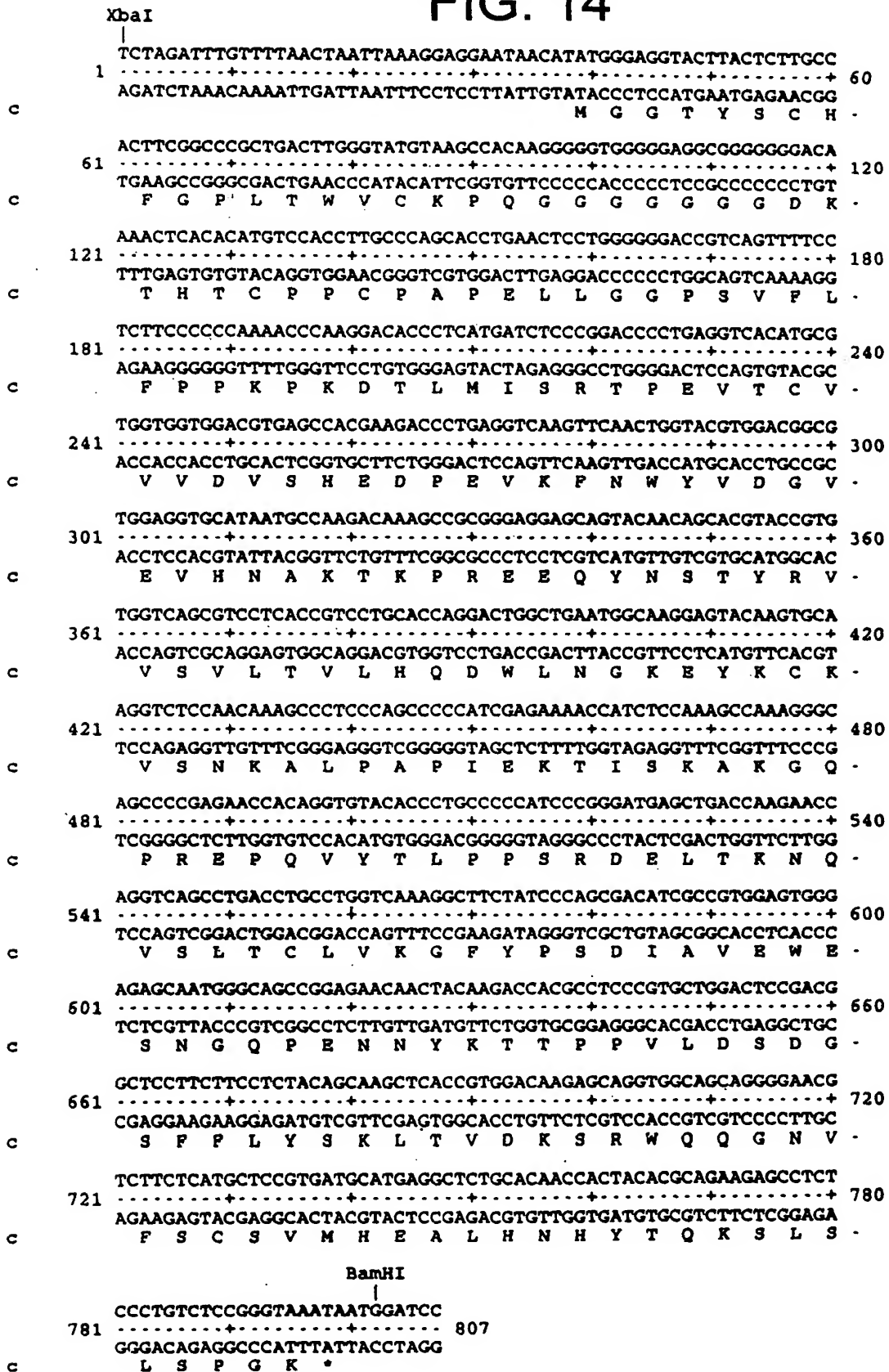


FIG. 16

XbaI
|
1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACACACATGTC 60
AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
M D K T H T C P -
c
61 CACCTTGCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCCTCTTCCCCCAAAC 120
GTGGAACGGGTGCTGGACTTGAGGACCCCTGGCAGTCAAAAGGAGAAGGGGGTTTTG
P C P A P E L L G G P S V F L P P P K P -
c
121 CCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGA 180
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S -
c
181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATAATG 240
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A -
c
241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCCAGCGTCTCA 300
GGTTCGTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCGTCGAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T -
c
301 CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG 360
GGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTACGTTCCAGAGGTTGTTTC
V L H Q D W L N G K E Y K C K V S N K A -
c
361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420
GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q -
c
421 AGGTGTACACCCCTGCCTCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCT 480
TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C -
c
481 GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCGCTCG
L V K G F Y P S D I A V E W E S N G Q P -
c
541 CGGAGAACAACACTACAAGACCACGCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCT 600
GCCTCTTGTGATGTTCTGGTGGGAGGGACGACCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y -
c
601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660
TGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V -
c
661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA 720
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
M H E A L H N H Y T Q K S L S L S P G K -
c
721 AAGGTGGAGGTGGTGGCGGAGGTACTTACTTGTCCACTTCGGCCCACTGACTTGGGTTT 780
TTCCACCTCCACCACCGCTCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCCAAA
G G G G G G G T Y S C H F G P L T W V C -
c
781 GCAAACCGCAGGGTGGCGGGCGGGCGGGGGTGGTACCTATTCTGTCTATTTGGCCCCG 840
CGTTTGGCGTCCACCGCCCGCGCGCCGCGCCACCATGGATAAGGACAGTAAACCGGGCG
K P Q G G G G G G G G T Y S C H F G P L -
c
BamHI
|
841 TGACCTGGGTATGTAAGCCACAAGGGGGTTAATCTCGAGGATCC 884
ACTGGACCCATACATTGGTGTTCCTCCCAATTAGAGCTCCTAGG
T W V C K P Q G G -

FIG. 17A

[AatII sticky end]
(position #4358 in pAMG21)

5' GCGTAACGTATGCATGGTCTCC -
3' TGCACGCATTGCATACGTACCAGAGG -

- CCATGCGAGAGTAGGGAAGTCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT -
- GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA -

- GGGCCTTTCGTTTTATCTGTTGTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC -
- CCCGAAAGCAAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCG -

- CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCCG -
- GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCCTCCACCGCCCGTCTGCGGGCG -

- CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGT -
- GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA -

AatII

- TTCTACAAACTCTTTTGTTTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC -
- AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG -

- TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAATTGCTTTAGAAATACTTTGGCAGC -
- AAAATTTACATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG -

- GGTGTTGTTGATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC -
- CCAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCAGCGGAATG -

- TACAGCCTAATATTTTGAATATCCCAAGAGCTTTTTCCTTCGCATGCCACGCTAAAC -
- ATGTCGGATTATAAAAACCTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTG -

- ATTCTTTTTCTCTTTTGTTTAAATCGTTGTTTGATTTATTATTTGCTATATTTATTTTC -
- TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAG -

- GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA -
- CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT -

- AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAAACTAAGCATTCCGAAGCCATTAT -
- TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTTCGTAAGGCTTCGGTAATA -

- TAGCAGTATGAATAGGGAAGCTAAACCCAGTGATAAGACCTGATGATTTGCTTCTTTAA -
- ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAAT -

- TTACATTTGGAGATTTTATTTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG -
- AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC -

- AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT -
- TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAATAATTTAATCGCAGTAGTA -

- AATATTGCCTCCATTTTATAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG -
- TTATAACGGAGGTAAAAATCCCATTAATAGGTCTTAACCTTTATAGTCTAAATTGGTATC -

- AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG -
- TTACTCCTATTTACTAGCGCTCATTATTATAAGTGTTACATGGTAAATCAGTATAGTC -

- ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT -
- TATTCGTAACATAATTATAGTAATAACGAAGATGTCCGAAATTAAAAATAATTAATAAGACA -

- AAGTGTCGTCGGCATTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTG -
- TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG -

- GCAAGTTTTGCGTGTTATATATCATTTAAACGGTAATAGATTGACATTTGATTCTAATAA -
- CGTTCAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT -

FIG. 17B

- ATTGGATTTTGTGCACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG -
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -
- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTGATT -
- ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -
- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -
- GATCTAAACAAAATTGATTAATTTCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -
- GCTCACTAGTGTGCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -
- GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -
- CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -
- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG -
- TGATCGTATTGGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -
- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

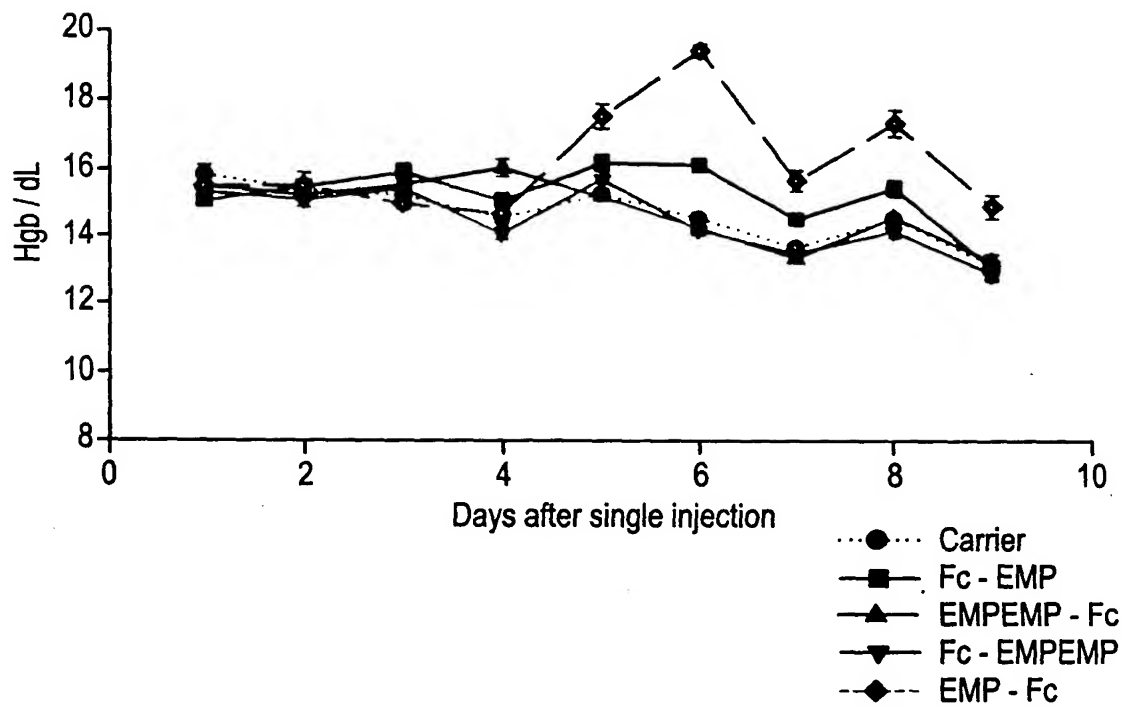


FIG.18A - 2

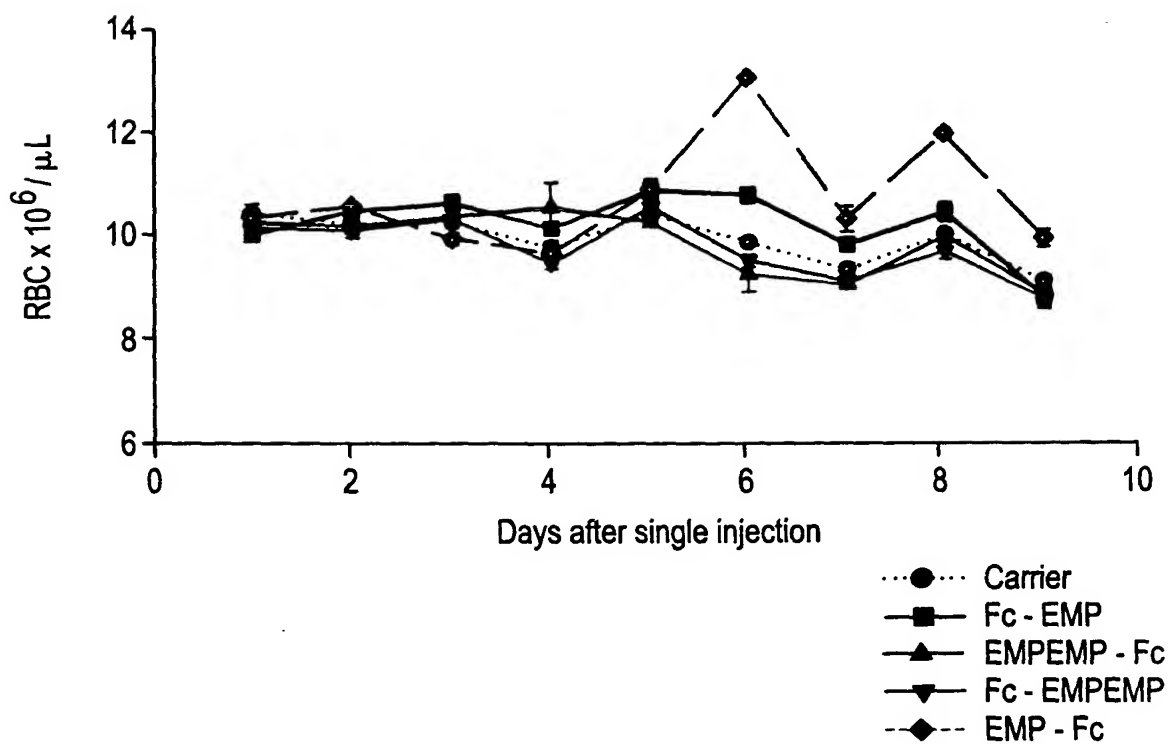


FIG.18A - 3

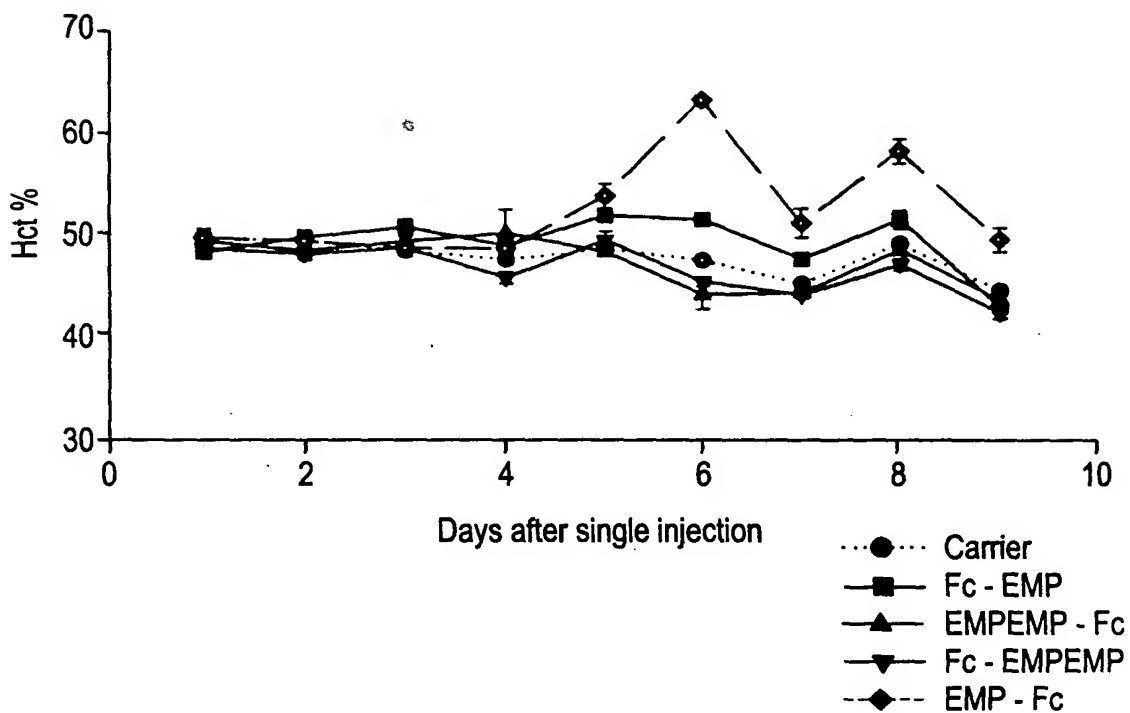


FIG.18B - 1

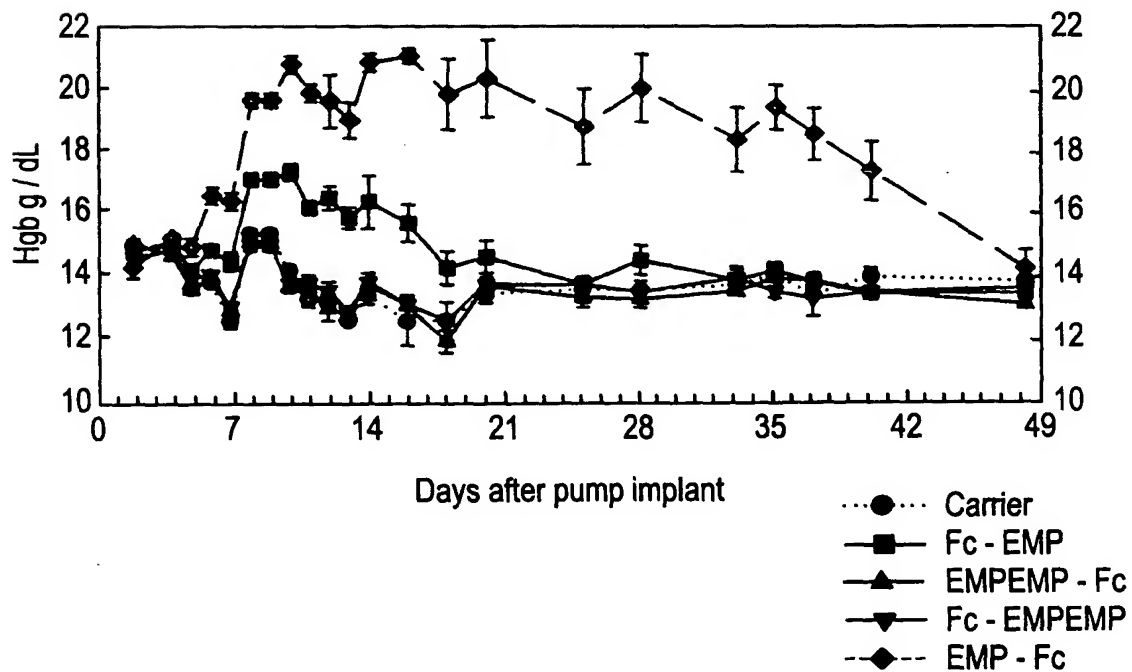


FIG.18B - 2

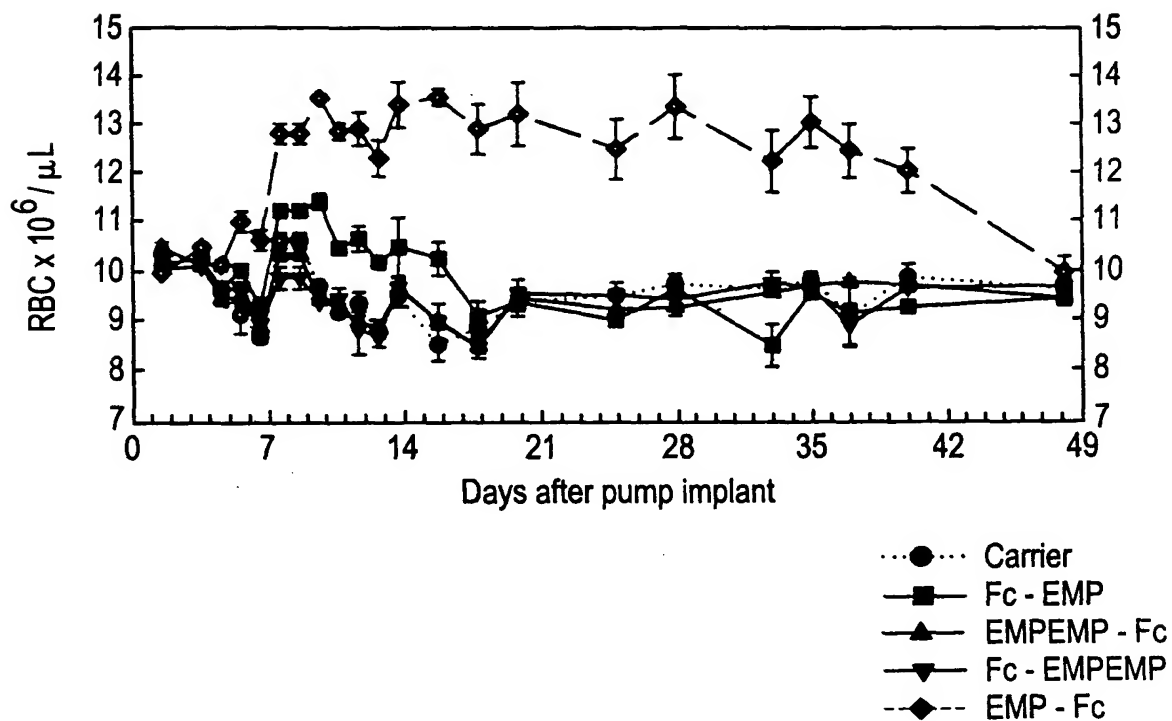


FIG.18B - 3

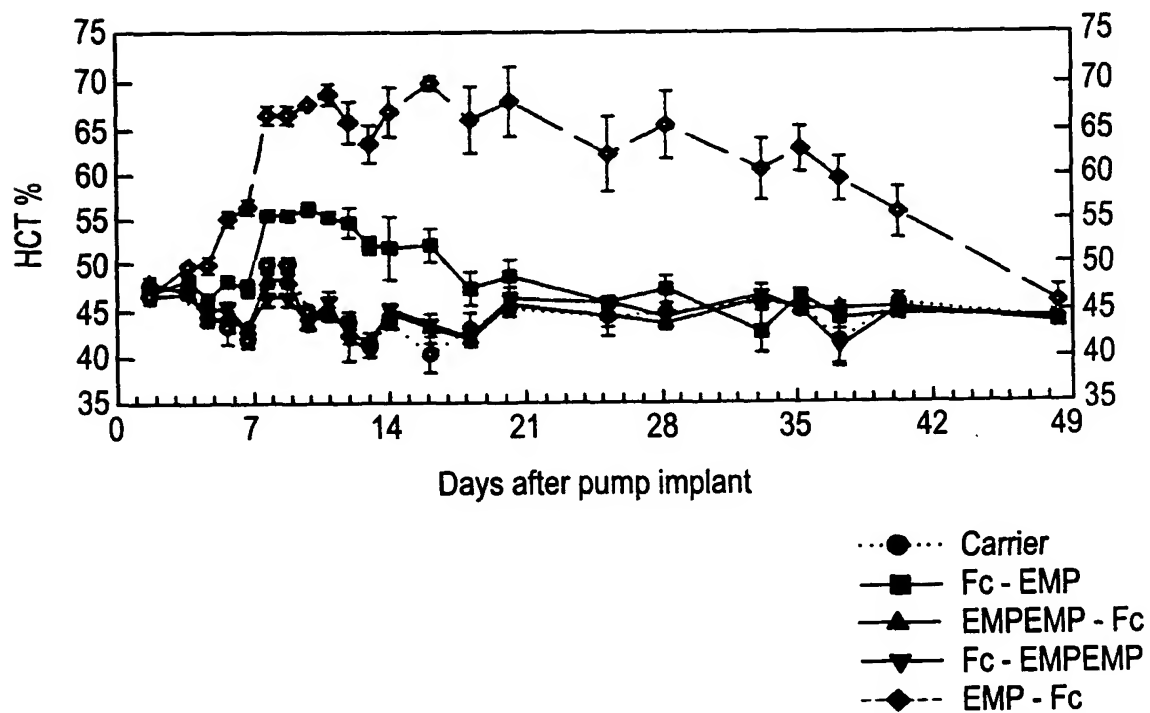


FIG. 19A

NdeI
|
1 CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG
-----+-----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
61 -----+-----+-----+-----+-----+-----+-----+ 120
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
121 -----+-----+-----+-----+-----+-----+-----+ 180
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTCGGCGCCCTCCTCGTCATGTTGTGC
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCCTACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCCTGACCGACTTACCGTTCCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA
301 -----+-----+-----+-----+-----+-----+-----+ 360
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
361 -----+-----+-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGTTTCTTGGTCCAGTCGGAAGTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTG
481 -----+-----+-----+-----+-----+-----+-----+ 540
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCAGCAG
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 19B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
    .....+.....+.....+.....+.....+.....+.....+
    GTCCCCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

    AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC
661 .....+.....+.....+.....+.....+.....+.....+ 720
    TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  D  F  L  P  H  Y  -

                                BamHI
                                |
    AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC
721 .....+.....+.....+.....+.....+.....+ 757
    TTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a      K  N  T  S  L  G  H  R  P  *
```

FIG. 20A

NdeI
|
CATATGGACTTCCTGCCGCACTACAAAAACACCTCTCTGGGTACACCGTCCGGGTGGAGGC
1+.....+.....+.....+.....+.....+.....+ 60
GTATACCTGAAGGACGGCGTGATGTTTTTGTGGAGAGACCCAGTGGCAGGCCCACCTCCG

a M D F L P H Y K N T S L G H R P G G G -

GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
61+.....+.....+.....+.....+.....+.....+ 120
CCACCCCTGTTTGTAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCCCTGGC

a G G D K T H T C P P C P A P E L L G G P -

TCAGTTTTCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCCCGACCCCTGAG
121+.....+.....+.....+.....+.....+.....+ 180
AGTCAAAAGGAGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
181+.....+.....+.....+.....+.....+.....+ 240
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
241+.....+.....+.....+.....+.....+.....+ 300
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
301+.....+.....+.....+.....+.....+.....+ 360
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA
361+.....+.....+.....+.....+.....+.....+ 420
ATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCTGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
421+.....+.....+.....+.....+.....+.....+ 480
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
481+.....+.....+.....+.....+.....+.....+ 540
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
541+.....+.....+.....+.....+.....+.....+ 600
CACCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

FIG. 20B

```
601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAG 660
-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a   D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 720
-----+-----+-----+-----+-----+
GTCCCCCTTG CAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG 761
-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC

a   K S L S L S P G K *
```

FIG. 21A

NdeI
|
CATATGGACAAAACCTCACACATGTCCACCTTGTCAGCTCCGGAACCTCTGGGGGGACCG
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
61 -----+-----+-----+-----+-----+-----+-----+ 120
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
121 -----+-----+-----+-----+-----+-----+-----+ 180
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCCTGACCGACTTACCGTTCCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA
301 -----+-----+-----+-----+-----+-----+-----+ 360
ATGTTACAGTTCCAGAGGTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
361 -----+-----+-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGTTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
481 -----+-----+-----+-----+-----+-----+-----+ 540
CACCTCACCCCTCTCGTTACCCGTGCGCCTCTTGTGATGTTCTGGTGGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

GACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 21B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  .

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  F  E  W  T  P  G  .

                                     BamHI
                                     |
721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
-----+-----+-----+-----+-----+ 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a      Y  W  Q  P  Y  A  L  P  L  *
```

FIG. 22A

NdeI
 |
 CATATGTTTGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG
 a M F E W T P G Y W Q P Y A L P L G G G -
 GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCTGGC
 a G G D K T H T C P P C P A P E L L G G P -
 TCAGTTTTCTCTTCCCCCAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAG
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
 a S V F L F P P K P K D T L M I S R T P E -
 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 CAGTGATACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
 a V T C V V V D V S H E D P E V K F N W Y -
 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC
 a V D G V E V H N A K T K P R E E Q Y N S -
 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCCTC
 a T Y R V V S V L T V L H Q D W L N G K E -
 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
 a Y K C K V S N K A L P A P I E K T I S K -
 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
 a A K G Q P R E P Q V Y T L P P S R D E L -
 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 TGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG
 a T K N Q V S L T C L V K G F Y P S D I A -
 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGGCACGAC
 a V E W E S N G Q P E N N Y K T T P P V L -

FIG. 22B

```
601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a   D S D G S F F L Y S K L T V D K S R W Q -
661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 720
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a   Q G N V F S C S V M H E A L H N H Y T Q -
                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
-----+-----+-----+-----+-----+ 757
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a   K S L S L S P G K *
```

FIG. 23A

NdeI
 |
 1 CATATGGACAAACTCACACATGTCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCG 60
 -----+-----+-----+-----+-----+
 GTATACCTGTTTGTAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC
 a M D K T H T C P P C P A P E L L G G P -
 61 TCAGTTTTCCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
 -----+-----+-----+-----+-----+
 AGTCAAAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
 a S V F L F P P K P K D T L M I S R T P E -
 121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
 -----+-----+-----+-----+-----+
 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
 a V T C V V V D V S H E D P E V K F N W Y -
 181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
 -----+-----+-----+-----+-----+
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC
 a V D G V E V H N A K T K P R E E Q Y N S -
 241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
 -----+-----+-----+-----+-----+
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
 a T Y R V V S V L T V L H Q D W L N G K E -
 301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
 -----+-----+-----+-----+-----+
 ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
 a Y K C K V S N K A L P A P I E K T I S K -
 361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
 -----+-----+-----+-----+-----+
 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
 a A K G Q P R E P Q V Y T L P P S R D E L -
 421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
 -----+-----+-----+-----+-----+
 TGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG
 a T K N Q V S L T C L V K G F Y P S D I A -
 481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG 540
 -----+-----+-----+-----+-----+
 CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCAGCAG
 a V E W E S N G Q P E N N Y K T T P P V L -
 541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
 -----+-----+-----+-----+-----+
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
 a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 23B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+
a   Q G N V F S C S V M H E A L H N H Y T Q -
    AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC
661 -----+-----+-----+-----+-----+-----+ 720
    TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTGGCTTGACACTG
a   K S L S L S P G K G G G G G V E P N C D -
                                     BamHI
                                     |
721 ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACCTCGAGGATCC 773
    TAGGTACAATACACCCTTACCCTTACAAAACCTTGCAGACATTGAGCTCCTAGG
a   I H V M W E W E C F E R L *
```

FIG. 24A

NdeI
|

```

1  CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT 60
   +-----+-----+-----+-----+-----+-----+
a  M V E P N C D I H V M W E W E C F E R .
   CTGGGTGGTGGTGGTGGTGACAAAACCTCACACATGTCCACCGTGCCCAGCACCTGAACCTC
61 +-----+-----+-----+-----+-----+-----+ 120
   GACCCACCACCACCACCCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAG
a  L G G G G G D K T H T C P P C P A P E L .
   CTGGGGGGACCGTCAGTTTTCTCTTCCCCCAAACCAAGGACACCCCTCATGATCTCC
121 +-----+-----+-----+-----+-----+-----+ 180
   GACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGG
a  L G G P S V F L F P P K P K D T L M I S .
   CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAG
181 +-----+-----+-----+-----+-----+-----+ 240
   GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC
a  R T P E V T C V V V D V S H E D P E V K .
   TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
241 +-----+-----+-----+-----+-----+-----+ 300
   AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC
a  F N W Y V D G V E V H N A K T K P R E E .
   CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
301 +-----+-----+-----+-----+-----+-----+ 360
   GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC
a  Q Y N S T Y R V V S V L T V L H Q D W L .
   AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA
361 +-----+-----+-----+-----+-----+-----+ 420
   TTACCGTTCCTCATGTTTCAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT
a  N G K E Y K C K V S N K A L P A P I E K .
   ACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
421 +-----+-----+-----+-----+-----+-----+ 480
   TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG
a  T I S K A K G Q P R E P Q V Y T L P P S .
   CGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCC
481 +-----+-----+-----+-----+-----+-----+ 540
   GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG
a  R D E L T K N Q V S L T C L V K G F Y P .
   AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACG
541 +-----+-----+-----+-----+-----+-----+ 600
   TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC
a  S D I A V E W E S N G Q P E N N Y K T T .

```


FIG. 24B

```

601 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
-----+-----+-----+-----+-----+-----+ 660
GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTC
a   P P V L D S D G S F F L Y S K L T V D K -
661 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
-----+-----+-----+-----+-----+-----+ 720
TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
a   S R W Q Q G N V F S C S V M H E A L H N -
                                     BamHI
                                     |
721 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC
-----+-----+-----+-----+-----+-----+ 773
GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG
a   H Y T Q K S L S L S P G K *
```

FIG. 25A

NdeI
|
CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTGTAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

TCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
61 -----+-----+-----+-----+-----+-----+-----+ 120
AGTCAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
121 -----+-----+-----+-----+-----+-----+-----+ 180
CAGTGTACGCACCACCACCTGCACCTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTTGACCGACTTACCGTTCTCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
301 -----+-----+-----+-----+-----+-----+-----+ 360
ATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
361 -----+-----+-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTG
481 -----+-----+-----+-----+-----+-----+-----+ 540
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 25B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCACTGGGGT
-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA

A      K  S  L  S  L  S  P  G  K  G  G  G  G  G  C  T  T  H  W  G  -

      BamHI
      |
721 TTCACCCTGTGCTAATGGATCCCTCGAG
-----+-----+-----+-----+ 748
AAGTGGGACACGATTACCTAGGGAGCTC

a      F  T  L  C  *
```

FIG. 26A

NdeI
|
CATATGTGCACCACCCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT
1+.....+.....+.....+.....+.....+.....+ 60
GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA

a M C T T H W G F T L C G G G G G D K G -

GGAGGCGGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG
61+.....+.....+.....+.....+.....+.....+ 120
CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTGCTGGACTTGAGGACCCC

a G G G G D K T H T C P P C P A P E L L G -

GGACCGTCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACC
121+.....+.....+.....+.....+.....+.....+ 180
CCTGGCAGTCAAAGGAGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG

a G P S V F L F P P K P K D T L M I S R T -

CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
181+.....+.....+.....+.....+.....+.....+ 240
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG

a P E V T C V V V D V S H E D P E V K F N -

TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC
241+.....+.....+.....+.....+.....+.....+ 300
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG

a W Y V D G V E V H N A K T K P R E E Q Y -

AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC
301+.....+.....+.....+.....+.....+.....+ 360
TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG

a N S T Y R V V S V L T V L H Q D W L N G -

AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
361+.....+.....+.....+.....+.....+.....+ 420
TTCTCATGTTTCAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG

a K E Y K C K V S N K A L P A P I E K T I -

TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT
421+.....+.....+.....+.....+.....+.....+ 480
AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTA

a S K A K G Q P R E P Q V Y T L P P S R D -

GAGCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
481+.....+.....+.....+.....+.....+.....+ 540
CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTG

a E L T K N Q V S L T C L V K G F Y P S D -

ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCC
541+.....+.....+.....+.....+.....+.....+ 600
TAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGGGAGGG

a I A V E W E S N G Q P E N N Y K T T P P -

FIG. 26B

```

601 GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
-----+-----+-----+-----+-----+-----+ 660
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC
a   V L D S D G S F F L Y S K L T V D K S R -
661 TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
-----+-----+-----+-----+-----+-----+ 720
ACCGTCGTCCCCCTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a   W Q Q G N V F S C S V M H E A L H N H Y -
                                     BamHI
                                     |
721 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
-----+-----+-----+-----+-----+ 763
TGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a   T Q K S L S L S P G K *
```